SEQUENCE LISTING

<110> MILLENNIUM PHARMACEUTICALS, INC.
      Cook, William
      Kapeller-Libermann, Rosana

<120> 14790, NOVEL PROTEIN KINASE MOLECULE AND
      USES TREREFOR

<130> 38155-20002.00

<140> US 09/515,806
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<160> 33

<170> FastSEQ for Windows Version 4.0

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   Met Ala Gly Gly Arg Gly Ala Pro Gly Arg Gly Arg Asp Glu Pro
   1               5                   10                  15

ccg gag agc tac ccg caa cga cag gac cac gag cta cag gcc ctg gag      155
Pro Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu
                 20                  25                  30

gcc atc tac ggc gcg gac ttc caa gac ctg cgg ccg gac gct tgc gga      203
Ala Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly
                 35                  40                  45

ccg gtc aaa gag ccc cct gaa atc aat tta gtt ttg tac cct caa ggc      251
Pro Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly
             50                  55                  60

cta act ggt gaa gaa gta tat gta aaa gtg gat ttg agg gtt aaa tgc      299
Leu Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys
         65                  70                  75

cca cct acc tat cca gat gta gtt cct gaa ata gag tta aaa aat gcc      347
Pro Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala
80                  85                  90                  95

aaa ggt cta tca aat gaa agt gtc aat ttg tta aaa tct cgc cta gaa      395
Lys Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu
                100                 105                 110
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gaa ctg gcc aag aaa cac tgt ggg gag gtg atg atc ttt gaa ctg gct        443
Glu Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala
            115                 120                 125

tac cac gtg cag tca ttt ctc agc gag cat aac aag ccc cct ccc aag        491
Tyr His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys
            130                 135                 140

tct ttt cat gaa gaa atg ctg gaa agg cgg gct cag gag gag cag cag        539
Ser Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln
            145                 150                 155

agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc        587
Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile
160                 165                 170                 175

ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa        635
Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys
                180                 185                 190

agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca        683
Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser
                195                 200                 205

aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct        731
Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala
            210                 215                 220

gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat        779
Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His
        225                 230                 235

cgg gca aac tcc tca gga agg tct agg cga gaa cgt cag tat tct gta        827
Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val
240                 245                 250                 255

tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat        875
Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn
                260                 265                 270

atg ggg agt cct gat cag ctc atg gtg cac aaa ggg aaa tgt att ggc        923
Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly
            275                 280                 285

agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc        971
Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala
            290                 295                 300

act ggt ggc ttt gtc ttg ttg tat gag tgg gtc ctt cag tgg cag aaa        1019
Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys
        305                 310                 315

aaa atg ggt cca ttc ctt acc agt caa gaa aaa gag aag att gat aag        1067
Lys Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys
320                 325                 330                 335

tgc aaa aag cag att caa gga aca gaa aca gaa ttc aac tca ctg gta        1115
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2

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Cys Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val
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aaa ttg agc cat cca aat gta gta cgc tac ctt gca atg aat ctc aaa    1163
Lys Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys
             355             360             365

gag caa gac gac tcc atc gtg gtg gac att tta gtg gag cac att agt    1211
Glu Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser
             370             375             380

ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg    1259
Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val
             385             390             395

cat cag ctt cgc agg tac aca gct cag ctc ctg tca ggc ctt gat tat    1307
His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr
400             405             410             415

ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc    1355
Leu His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val
             420             425             430

ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct    1403
Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser
             435             440             445

aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga    1451
Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg
             450             455             460

gtt cgt ttt agt gac aat gct ctg cct tat aaa acg ggg aag aaa gga    1499
Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly
             465             470             475

gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag    1547
Asp Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln
480             485             490             495

gaa tgt gga gag tac cct gtg acc atc cct agt gac tta cca gct gac    1595
Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp
             500             505             510

ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga    1643
Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg
             515             520             525

tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca    1691
Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro
             530             535             540

aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat    1739
Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp
             545             550             555

tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc    1787
Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe
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3

ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa   1835
Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu
            580   585   590

gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg   1883
Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val
            595   600   605

cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc   1931
Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile
            610   615   620

aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg   1979
Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu
            625   630   635

ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg   2027
Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp
640   645   650   655

atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac   2075
Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp
                660   665   670

tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg   2123
Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala
                675   680   685

agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc   2171
Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro
            690   695   700

atc ctc agc agc tcg gtg gag tgg agc act tcg ggc gag cgc tcg gcc   2219
Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala
705   710   715

agt gcc cgt ttc ccc gcc acc ggc ccg ggc tcc agc gat gac gag gac   2267
Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp
720   725   730   735

gac gac gag gac gag cac ggt ggc gtc ttc tcc cag tcc ttc ctg cct   2315
Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro
                740   745   750

gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac   2363
Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn
            755   760   765

agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat ggc tgc   2411
Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys
            770   775   780

cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac   2459
His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr
785   790   795

4

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atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac      2507
Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp
800             805             810             815

cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag      2555
Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu
            820             825             830

att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac cgg      2603
Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg
            835             840             845

gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa      2651
Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys
            850             855             860

ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac      2699
Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp
        865             870             875

agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca      2747
Ser Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser
880             885             890             895

ggt cac tta act ggg atg gtt ggc act gct ctc tat gta agc cca gag      2795
Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu
            900             905             910

gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc      2843
Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe
            915             920             925

agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg      2891
Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr
            930             935             940

gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg      2939
Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser
        945             950             955

cct aag ttt cca gaa gac ttt gac gat gga gag cat gca aag cag aaa      2987
Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys
960             965             970             975

tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca      3035
Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr
            980             985             990

gcc aca gaa ctg ctc aag agt gag ctg ctg ccc cca ccc cag atg gag      3083
Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu
                995             1000            1005

gag tca gag ctg cat gaa gtg ctg cac cac acg ctg acc aac gtg gat      3131
Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp
            1010            1015            1020
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5

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ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc    3179
Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile
    1025                1030                1035

tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac    3227
Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn
1040                1045                1050                1055

ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc    3275
Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile
                1060                1065                1070

atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta    3323
Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu
                1075                1080                1085

ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta    3371
Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu
                1090                1095                1100

ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg    3419
Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg
                1105                1110                1115

atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa    3467
Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys
1120                1125                1130                1135

cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt    3515
Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe
                1140                1145                1150

cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc    3563
His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr
                1155                1160                1165

acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa    3611
Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
                1170                1175                1180

atc atc caa gag ttt cca gca ctt cag gaa aga aat tac agt att tat    3659
Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr
    1185                1190                1195

ttg aac cat acc atg tta ttg aaa gca ata ctc tta cac tgt ggg atc    3707
Leu Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile
1200                1205                1210                1215

cca gaa gat aaa ctc agt caa gtc tac att att ctg tat gat gct gtg    3755
Pro Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val
                1220                1225                1230

aca gag aag ctg acg agg aga gaa gtg gaa gct aaa ttt tgt aat ctg    3803
Thr Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu
                1235                1240                1245

tct ttg tct tct aat agt ctg tgt cga ctc tac aag ttt att gaa cag    3851
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6

Ser Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln
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aag gga gat ttg caa gat ctt atg cca aca ata aat tca tta ata aaa   3899
Lys Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys
        1265   1270   1275

cag aaa aca ggt att gca cag ttg gtg aag tat ggc tta aaa gac cta   3947
Gln Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu
1280   1285   1290   1295

gag gag gtt gtt gga ctg ttg aag aaa ctc ggc atc aag tta cag gtc   3995
Glu Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val
                1300   1305   1310

ttg atc aat ttg ggc ttg gtt tac aag gtg cag cag cac aat gga atc   4043
Leu Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile
                1315   1320   1325

atc ttc cag ttt gtg gct ttc atc aaa cga agg caa agg gct gta cct   4091
Ile Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro
            1330   1335   1340

gaa atc ctc gca gct gga ggc aga tat gac ctg ctg att ccc cag ttt   4139
Glu Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe
        1345   1350   1355

aga ggg cca caa gct ctg ggg cca gtt ccc act gcc att ggg gtc agc   4187
Arg Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser
1360   1365   1370   1375

ata gct ata gac aag ata tct gct gct gtc ctc aac atg gag gaa tct   4235
Ile Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser
                1380   1385   1390

gtt aca ata agc tct tgt gac ctc ctg gtt gta agt gtt ggt cag atg   4283
Val Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met
            1395   1400   1405

tct atg tcc agg gcc atc aac cta acc cag aaa ctc tgg aca gca ggc   4331
Ser Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly
        1410   1415   1420

atc aca gca gaa atc atg tac gac tgg tca cag tcc caa gag gaa tta   4379
Ile Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu
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caa gag tac tgc aga cat cat gaa atc acc tat gtg gcc ctt gtc tcg   4427
Gln Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser
1440   1445   1450   1455

gat aaa gaa gga agc cat gtc aag gtt aag tct ttc gag aag gaa agg   4475
Asp Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg
                1460   1465   1470

cag aca gag aag cgt gtg ctg gag act gaa ctt gtg gac cat gta ctg   4523
Gln Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu

7

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                1475                 1480                 1485

cag aaa ctg agg act aaa gtc act gat gaa agg aat ggc aga gaa gct      4571
Gln Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala
        1490                 1495                 1500


tcc gat aat ctt gca gtg caa aat ctg aag ggg tca ttt tct aat gct      4619
Ser Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala
        1505                 1510                 1515


tca ggt ttg ttt gaa atc cat gga gca aca gtg gtt ccc att gtg agt      4667
Ser Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser
1520                 1525                 1530                 1535


gtg cta gcc ccg gag aag ctg tca gcc agc act agg agg cgc tat gaa      4715
Val Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu
                1540                 1545                 1550


act cag gta caa act cga ctt cag acc tcc ctt gcc aac tta cat cag      4763
Thr Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln
                1555                 1560                 1565


aaa agc agt gaa att gaa att ctg gct gtg gat cta ccc aaa gaa aca      4811
Lys Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr
        1570                 1575                 1580


ata tta cag ttt tta tca tta gag tgg gat gct gat gaa cag gca ttt      4859
Ile Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe
        1585                 1590                 1595


aac aca act gtg aag cag ctg ctg tca cgc ctg cca aag caa aga tac      4907
Asn Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr
1600                 1605                 1610                 1615


ctc aaa tta gtc tgt gat gaa att tat aac atc aaa gta gaa aaa aag      4955
Leu Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys
                1620                 1625                 1630


gtg tct gtg cta ttt ctg tac agc tat aga gat gac tac tac aga atc      5003
Val Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile
        1635                 1640                 1645


tta ttt taa ccctaaagaa ctgtcgttaa cctcattcaa acagacagag              5052
Leu Phe  *


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8

<212> PRT
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Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly Pro
        35             40             45
Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
    50             55             60
Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys Pro
65             70             75             80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
            85             90             95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu Glu
            100            105            110
Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala Tyr
        115            120            125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130            135            140
Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln Arg
145            150            155            160
Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
            165            170            175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180            185            190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser Asn
        195            200            205
Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala Ala
    210            215            220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His Arg
225            230            235            240
Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
            245            250            255
Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn Met
            260            265            270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly Ser
    275            280            285
Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290            295            300
Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys Lys
305            310            315            320
Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys
            325            330            335
Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val Lys
            340            345            350
Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys Glu
            355            360            365
Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser Gly
    370            375            380
Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val His
385            390            395            400
Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr Leu
            405            410            415
His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val Leu
```

9

```
                    420                          425                          430
Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys
            435                          440                          445
Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg Val
        450                          455                          460
Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp
465                          470                          475                          480
Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu
                        485                          490                          495
Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe
                    500                          505                          510
Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp
            515                          520                          525
Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys
        530                          535                          540
Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr
545                          550                          555                          560
Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe Phe
                        565                          570                          575
Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu
                    580                          585                          590
Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln
            595                          600                          605
Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn
        610                          615                          620
Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu
625                          630                          635                          640
Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile
                        645                          650                          655
Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp Ser
                    660                          665                          670
Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala Ser
            675                          680                          685
Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro Ile
        690                          695                          700
Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala Ser
705                          710                          715                          720
Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp Asp
                        725                          730                          735
Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro Ala
                    740                          745                          750
Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser
            755                          760                          765
Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys His
        770                          775                          780
Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr Ile
785                          790                          795                          800
Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln
                        805                          810                          815
Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu Ile
                    820                          825                          830
Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp
            835                          840                          845
Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile
        850                          855                          860
Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp Ser
865                          870                          875                          880
```

10

```
Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser Gly
            885                     890                 895
His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val
            900                     905                 910
Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser
            915                     920                 925
Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala
            930                     935                 940
Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro
945                     950                 955                 960
Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys Ser
                965                     970                 975
Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala
                980                     985                 990
Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu
            995                     1000                1005
Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp Gly
            1010                    1015                1020
Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile Ser
1025                    1030                1035                1040
Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe
                1045                    1050                1055
Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile Ile
                1060                    1065                1070
Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu
                1075                    1080                1085
Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe
                1090                    1095                1100
Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile
1105                    1110                1115                1120
Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg
                1125                    1130                1135
Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His
                1140                    1145                1150
Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr
                1155                    1160                1165
Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile
                1170                    1175                1180
Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu
1185                    1190                1195                1200
Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro
                1205                    1210                1215
Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr
                1220                    1225                1230
Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser
                1235                    1240                1245
Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys
                1250                    1255                1260
Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln
1265                    1270                1275                1280
Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu
                1285                    1290                1295
Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu
                1300                    1305                1310
Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile
                1315                    1320                1325
Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu
```

11

```
          1330                    1335                   1340
Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg
1345                    1350                   1355                   1360
Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile
               1365                   1370                  1375
Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val
          1380                    1385                  1390
Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser
          1395                    1400                  1405
Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile
     1410                    1415                  1420
Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln
1425                    1430                   1435                   1440
Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp
               1445                   1450                  1455
Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln
               1460                   1465                  1470
Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu Gln
          1475                    1480                  1485
Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser
          1490                    1495                  1500
Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser
1505                    1510                   1515                   1520
Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser Val
               1525                   1530                  1535
Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr
          1540                    1545                  1550
Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys
          1555                    1560                  1565
Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile
     1570                    1575                  1580
Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn
1585                    1590                   1595                   1600
Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu
               1605                   1610                  1615
Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val
          1620                    1625                  1630
Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu
          1635                    1640                  1645
Phe
```

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<210> 3
<211> 4950
<212> DNA
<213> Homo sapiens

<400> 3
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caacgacagg accacgagct acaggccctg gaggccatct acggcgcgga cttccaagac     120
ctgcggccgg acgcttgcgg accggtcaaa gagcccctg aaatcaattt agttttgtac     180
cctcaaggcc taactggtga agaagtatat gtaaaagtgg atttgagggt taaatgccca     240
cctacctatc cagatgtagt tcctgaaata gagttaaaaa atgccaaagg tctatcaaat     300
gaaagtgtca atttgttaaa atctcgccta gaagaactgg ccaagaaaca ctgtggggag     360
gtgatgatct ttgaactggc ttaccacgtg cagtcatttc tcagcgagca taacaagccc     420
cctcccaagt cttttcatga agaaatgctg gaaaggcggg ctcaggagga gcagcagagg     480
ctgttggagg ccaagcggaa agaagagcag gagcaacgtg aaatcctgca tgagattcag     540
```

```
agaaggaaag aagagataaa agaagagaaa aaaaggaaag aaatggctaa gcaggaacgt    600
ttggaaattg ctagtttgtc aaaccaagat catacctcta agaaggaccc aggaggacac    660
agaacggctg ccattctaca tggaggctct cctgactttg taggaaatgg taaacatcgg    720
gcaaactcct caggaaggtc taggcgagaa cgtcagtatt ctgtatgtaa tagtgaagat    780
tctcctggct cttgtgaaat tctgtatttc aatatgggga gtcctgatca gctcatggtg    840
cacaaaggga aatgtattgg cagtgatgaa caacttggaa aattagtcta caatgctttg    900
gaaacagcca ctggtggctt tgtcttgttg tatgagtggg tccttcagtg gcagaaaaaa    960
atgggtccat tccttaccag tcaagaaaaa gagaagattg ataagtgcaa aaagcagatt   1020
caaggaacag aaacagaatt caactcactg gtaaaattga gccatccaaa tgtagtacgc   1080
taccttgcaa tgaatctcaa agagcaagac gactccatcg tggtggacat tttagtggag   1140
cacattagtg gggtctctct tgctgcacac ctgagccact caggccccat ccctgtgcat   1200
cagcttcgca ggtacacagc tcagctcctg tcaggccttg attatctgca cagcaattct   1260
gtggtgcata aggtcctgag tgcatctaat gtcttggtgg atgcagaagg caccgtcaag   1320
attacggact atagcatttc taagcgcctc gcagacattt gcaaggagga tgtgtttgag   1380
caaacccgag ttcgttttag tgacaatgct ctgccttata aaacggggaa gaaaggagat   1440
gtttggcgtc ttggccttct gctgctgtcc ctcagccaag gacaggaatg tggagagtac   1500
cctgtgacca tccctagtga cttaccagct gactttcaag attttctaaa gaaatgtgtg   1560
tgcttggatg acaaggaaag atggagtccc cagcagttgt tgaaacacag ctttatataat  1620
ccccagccaa aaatgcctct agtggaacaa agtcctgaag attctggagg acaagattat   1680
gttgagactg ttattcctag caaccggcta cccagtgctg ccttctttag tgagacacag   1740
agacagtttt cccgatactt cattgagttt gaagaattac aacttcttgg taaaggagct   1800
tttggagctg tcatcaaggt gcagaacaag ttggacggct gctgctacgc agtgaagcgc   1860
atccccatca acccggccag ccggcagttc cgcaggatca agggcgaagt gacactgctg   1920
tcacggctgc accatgagaa cattgtgcgc tactacaacg cctggatcga gcggcacgag   1980
cggccggcgg gaccggggac gccgcccccg gactccgggc ccctggccaa ggatgaccga   2040
gctgcacgcg ggcagccggc gagcgacaca gacggcctgg acagcgtaga ggccgccgcg   2100
ccgccaccca tcctcagcag ctcggtggag tggagcactt cgggcgagcg ctcggccagt   2160
gcccgtttcc ccgccaccgg cccgggctcc agcgatgacg aggacgacga cgaggacgag   2220
cacggtggcg tcttctccca gtccttcctg cctgcttcag attctgaaag tgatattatc   2280
tttgacaatg aagatgagaa cagtaaaagt cagaatcagg atgaagattg caatgaaaag   2340
aatggctgcc atgaaagtga gccatcagtg acgactgagg ctgtgcacta cctatacatc   2400
cagatggagt actgtgagaa gagcacttta cgagacacca ttgaccaggg actgtatcga   2460
gacaccgtca gactctggag gctttttcga gagattctgg atggattagc ttatatccat   2520
gagaaaggaa tgattcaccg ggatttgaag cctgtcaaca tttttttgga ttctgatgac   2580
catgtgaaaa taggtgattt tggttttggcg acagaccatc tagccttttc tgctgacagc   2640
aaacaagacg atcagacagg agacttgatt aagtcagacc cttcaggtca cttaactggg   2700
atggttggca ctgctctcta tgtaagccca gaggtccaag gaagcaccaa atctgcatac   2760
aaccagaaag tggatctctt cagcctggga attatcttct ttgagatgtc ctatcacccc   2820
atggtcacgg cttcagaaag gatctttgtt ctcaaccaac tcagagatcc cacttcgcct   2880
aagtttccag aagactttga cgatggagag catgcaaagc agaaatcagt catctcctgg   2940
ctgttgaacc acgatccagc aaaaacggccc acagccacag aactgctcaa gagtgagctg   3000
ctgcccccac cccagatgga ggagtcagag ctgcatgaag tgctgcacca cacgctgacc   3060
aacgtggatg ggaaggccta ccgcaccatg atgggcccaga tcttctcgca gcgcatctcc   3120
cctgccatcg attacaccta tgacagcgac atactgaagg gcaacttctc aatccgtaca   3180
gccaagatgc agcagcatgt gtgtgaaacc atcatccgca tctttaaaag acatggagct   3240
gttcagttgt gtactccact actgcttccc cgaaacagac aaatatatga gcacaacgaa   3300
gctgccctat tcatggacca cagcgggatg ctggtgatgc ttcctttttga cctgcggatc   3360
cctttttgcaa gatatgtggc aagaaataat atattgaatt taaaacgata ctgcatagaa   3420
cgtgtgttca ggccgcgcaa gttagatcga tttcatccca aagaacttct ggagtgtgca   3480
tttgatattg tcacttctac caccaacagc tttctgccca ctgctgaaat tatctacact   3540
atctatgaaa tcatccaaga gtttccagca cttcaggaaa gaaattacag tatttatttg   3600
aaccatacca tgttattgaa agcaatactc ttacactgtg ggatcccaga agataaactc   3660
agtcaagtct acattattct gtatgatgct gtgacagaga agctgacgag gagagaagtg   3720
gaagctaaat tttgtaatct gtctttgtct tctaatagtc tgtgtcgact ctacaagttt   3780
attgaacaga agggagattt gcaagatctt atgccaacaa taaattcatt aataaaacag   3840
aaaacaggta ttgcacagtt ggtgaagtat ggcttaaaag acctagagga ggttgttgga   3900
ctgttgaaga aactcggcat caagttacag gtcttgatca atttgggctt ggtttacaag   3960
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13

```
gtgcagcagc acaatggaat catcttccag tttgtggctt tcatcaaacg aaggcaaagg   4020
gctgtacctg aaatcctcgc agctggaggc agatatgacc tgctgattcc ccagtttaga   4080
gggccacaag ctctggggcc agttcccact gccattgggg tcagcatagc tatagacaag   4140
atatctgctg ctgtcctcaa catggaggaa tctgttacaa taagctcttg tgacctcctg   4200
gttgtaagtg ttggtcagat gtctatgtcc agggccatca acctaaccca gaaactctgg   4260
acagcaggca tcacagcaga aatcatgtac gactggtcac agtcccaaga ggaattacaa   4320
gagtactgca gacatcatga aatcacctat gtggcccttg tctcggataa agaaggaagc   4380
catgtcaagg ttaagtcttt cgagaaggaa aggcagacag agaagcgtgt gctggagact   4440
gaacttgtgg accatgtact gcagaaactg aggactaaag tcactgatga aaggaatggc   4500
agagaagctt ccgataatct tgcagtgcaa aatctgaagg ggtcattttc taatgcttca   4560
ggtttgtttg aaatccatgg agcaacagtg gttcccattg tgagtgtgct agccccggag   4620
aagctgtcag ccagcactag gaggcgctat gaaactcagg tacaaactcg acttcagacc   4680
tcccttgcca acttacatca gaaaagcagt gaaattgaaa ttctggctgt ggatctaccc   4740
aaagaaacaa tattacagtt tttatcatta gagtgggatg ctgatgaaca ggcatttaac   4800
acaactgtga agcagctgct gtcacgcctg ccaaagcaaa gatacctcaa attagtctgt   4860
gatgaaattt ataacatcaa agtagaaaaa aaggtgtctg tgctatttct gtacagctat   4920
agagatgact actacagaat cttattttaa                                     4950
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<210> 4
<211> 1648
<212> PRT
<213> Homo sapiens

<400> 4
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Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu Ala
                20              25              30
Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly Pro
            35              40              45
Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
        50              55              60
Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys Pro
65              70              75              80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                85              90              95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu Glu
            100             105             110
Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala Tyr
        115             120             125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130             135             140
Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln Arg
145             150             155             160
Leu Leu Glu Ala Arg Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165             170             175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180             185             190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Thr Ser Leu Ser Asn
        195             200             205
Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala Ala
    210             215             220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His Arg
225             230             235             240
Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
            245             250             255
```

14

```
Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn Met
            260                 265                 270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Arg Cys Ile Gly Ser
        275                 280                 285
Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290                 295                 300
Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys Met
305                 310                 315                 320
Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys Lys
                325                 330                 335
Lys Gln Ile Gln Gly Tyr Glu Thr Glu Phe Asn Ser Leu Val Lys Leu
                340                 345                 350
Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys Glu Gln
        355                 360                 365
Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser Gly Val
    370                 375                 380
Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val His Gln
385                 390                 395                 400
Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr Leu His
                405                 410                 415
Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val Leu Val
        420                 425                 430
Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys Arg
        435                 440                 445
Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg Val Arg
    450                 455                 460
Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp Val
465                 470                 475                 480
Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu Cys
                485                 490                 495
Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe Gln
            500                 505                 510
Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp Ser
            515                 520                 525
Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys Met
    530                 535                 540
Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr Val
545                 550                 555                 560
Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe Phe Ser
                565                 570                 575
Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu Leu
            580                 585                 590
Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln Asn
        595                 600                 605
Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn Pro
    610                 615                 620
Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu Ser
625                 630                 635                 640
Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile Glu
                645                 650                 655
Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp Ser Gly
            660                 665                 670
Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala Ser Asp
        675                 680                 685
Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro Ile Leu
    690                 695                 700
Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala Ser Ala
```

15

```
705                    710                   715                    720
Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp Asp Glu
                   725                   730                    735
Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro Ala Ser Asp
                   740                   745                   750
Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser Lys Ser
              755                   760                   765
Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys His Glu Ser
         770                   775                   780
Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr Ile Gln Met
    785                   790                   795                    800
Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln Gly Leu
                   805                   810                    815
Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu Ile Leu Asp
              820                   825                   830
Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp Leu Lys
         835                   840                   845
Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile Gly Asp
    850                   855                   860
Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp Ser Lys Gln
865                   870                   875                    880
Asp Asp Gln Thr Gly Asp Gly Leu Ile Lys Ser Asp Pro Ser Gly His
              885                   890                   895
Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val Gln
              900                   905                   910
Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser Leu
         915                   920                   925
Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala Ser
    930                   935                   940
Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro Lys
945                   950                   955                    960
Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys Ser Val
              965                   970                   975
Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala Thr
         980                   985                   990
Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu Ser
         995                   1000                  1005
Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp Gly Lys
    1010                  1015                  1020
Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile Ser Pro
1025                  1030                  1035                   1040
Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe Ser
              1045                  1050                  1055
Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile Ile Arg
         1060                  1065                  1070
Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu
    1075                  1080                  1085
Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met
    1090                  1095                  1100
Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile Pro
1105                  1110                  1115                   1120
Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr
              1125                  1130                  1135
Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
         1140                  1145                  1150
Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn
         1155                  1160                  1165
```

16

```
Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile Ile
    1170                1175                1180
Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn
1185                1190                1195                1200
His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu
            1205                1210                1215
Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr Glu
            1220                1225                1230
Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu
        1235                1240                1245
Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly
        1250                1255                1260
Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys
1265                1270                1275                1280
Thr Gly Ile Ala Gln Leu Val Lys Tyr Ser Leu Lys Asp Leu Glu Asp
            1285                1290                1295
Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu Ile
            1300                1305                1310
Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe
        1315                1320                1325
Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile
        1330                1335                1340
Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly
1345                1350                1355                1360
Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala
            1365                1370                1375
Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr
            1380                1385                1390
Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser Met
        1395                1400                1405
Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr
    1410                1415                1420
Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu
1425                1430                1435                1440
Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys
            1445                1450                1455
Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr
            1460                1465                1470
Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu Gln Lys
        1475                1480                1485
Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser Asp
    1490                1495                1500
Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly
1505                1510                1515                1520
Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser Val Leu
            1525                1530                1535
Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Ile Gln
            1540                1545                1550
Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser
        1555                1560                1565
Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu
    1570                1575                1580
Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr
1585                1590                1595                1600
Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys
            1605                1610                1615
Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser
```

17

```
                1620                    1625                    1630
    Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
            1635                    1640                    1645


<210> 5
<211> 1648
<212> PRT
<213> Mouse


<400> 5
Met Ala Gly Gly Arg Gly Ala Ser Gly Arg Gly Arg Ala Glu Pro Gln
1                   5                   10                  15
Glu Ser Tyr Ser Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu Ala
            20                  25                  30
Ile Tyr Gly Ser Asp Phe Gln Asp Leu Arg Pro Asp Ala Arg Gly Arg
            35                  40                  45
Val Arg Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
     50                  55                  60
Ala Gly Glu Glu Val Tyr Val Gln Val Glu Leu Gln Val Lys Cys Pro
65                  70                  75                  80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                85                  90                  95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser His Leu Glu Glu
            100                 105                 110
Leu Ala Lys Lys Gln Cys Gly Glu Val Met Ile Phe Glu Leu Ala His
            115                 120                 125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
     130                 135                 140
Phe His Glu Glu Met Leu Glu Arg Gln Ala Gln Glu Lys Gln Gln Arg
145                 150                 155                 160
Leu Leu Glu Ala Arg Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165                 170                 175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180                 185                 190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Thr Ser Leu Thr Asn
            195                 200                 205
Gln Asp Tyr Ala Ser Lys Arg Asp Pro Ala Gly His Arg Ala Ala Ala
     210                 215                 220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys Ala Arg
225                 230                 235                 240
Thr Tyr Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
                245                 250                 255
Ser Gly Glu Pro Ser Pro Gly Ser Cys Asp Ile Leu His Phe Ser Val
            260                 265                 270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Arg Cys Val Gly Ser
            275                 280                 285
Asp Glu Gln Leu Gly Lys Val Val Tyr Asn Ala Leu Glu Thr Ala Thr
     290                 295                 300
Gly Ser Phe Val Leu Leu His Glu Trp Val Leu Gln Trp Gln Lys Met
305                 310                 315                 320
Gly Pro Cys Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys Lys
                325                 330                 335
Arg Gln Ile Gln Gly Ala Glu Thr Glu Phe Ser Ser Leu Val Lys Leu
            340                 345                 350
Ser His Pro Asn Ile Val Arg Tyr Phe Ala Met Asn Ser Arg Glu Glu
     355                 360                 365
Glu Asp Ser Ile Val Ile Asp Ile Leu Ala Glu His Val Ser Gly Ile
```

18

```
              370                    375                    380
Ser Leu Ala Thr His Leu Ser His Ser Gly Pro Val Pro Ala His Gln
385                    390                    395                    400
Leu Arg Lys Tyr Thr Ala Gln Leu Leu Ala Gly Leu Asp Tyr Leu His
                  405                    410                    415
Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Ser Val Leu Val
                  420                    425                    430
Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys Arg
              435                    440                    445
Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Ala Arg Val Arg
              450                    455                    460
Phe Ser Asp Ser Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp Val
465                    470                    475                    480
Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu Cys
                  485                    490                    495
Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe Gln
              500                    505                    510
Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp Ser
              515                    520                    525
Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys Leu
              530                    535                    540
Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr Ile
545                    550                    555                    560
Glu Thr Val Ile Pro Ser Asn Gln Leu Pro Ser Ala Ala Phe Phe Ser
                  565                    570                    575
Glu Thr Gln Lys Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu Leu
              580                    585                    590
Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln Asn
              595                    600                    605
Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn Pro
              610                    615                    620
Ala Ser Arg His Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu Ser
625                    630                    635                    640
Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile Glu
                  645                    650                    655
Arg His Glu Arg Pro Ala Val Pro Gly Thr Pro Pro Asp Cys Thr
                  660                    665                    670
Pro Gln Ala Gln Asp Ser Pro Ala Thr Cys Gly Lys Thr Ser Gly Asp
              675                    680                    685
Thr Glu Glu Leu Gly Ser Val Glu Ala Ala Ala Pro Pro Pro Ile Leu
              690                    695                    700
Ser Ser Ser Val Glu Trp Ser Thr Ser Ala Glu Arg Ser Thr Ser Thr
705                    710                    715                    720
Arg Phe Pro Val Thr Gly Gln Asp Ser Ser Ser Asp Glu Glu Asp Glu
                  725                    730                    735
Asp Glu Arg Asp Gly Val Phe Ser Gln Ser Phe Leu Pro Ala Ser Asp
                  740                    745                    750
Ser Asp Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser Lys Ser
                  755                    760                    765
Gln Asn Gln Asp Glu Asp Cys Asn Gln Lys Asp Gly Ser His Glu Ile
              770                    775                    780
Glu Pro Ser Val Thr Ala Glu Ala Val His Tyr Leu Tyr Ile Gln Met
785                    790                    795                    800
Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln Gly Leu
                  805                    810                    815
Phe Arg Asp Thr Ser Arg Leu Trp Arg Leu Phe Arg Glu Ile Leu Asp
              820                    825                    830
```

19

```
Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp Leu Lys
        835                 840                 845
Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile Gly Asp
    850                 855                 860
Phe Gly Leu Ala Thr Asp His Leu Ala Phe Thr Ala Glu Gly Lys Gln
865                 870                 875                 880
Asp Asp Gln Ala Gly Asp Gly Val Ile Lys Ser Asp Pro Ser Gly His
                885                 890                 895
Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val Gln
                900                 905                 910
Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser Leu
    915                 920                 925
Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala Ser
    930                 935                 940
Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro Lys
945                 950                 955                 960
Phe Pro Asp Asp Phe Asp Asp Gly Glu His Thr Lys Gln Lys Ser Val
                965                 970                 975
Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala Met
                980                 985                 990
Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu Ser
    995                 1000                1005
Glu Leu His Glu Val Leu His His Thr Leu Ala Asn Ile Asp Gly Lys
    1010                1015                1020
Ala Tyr Arg Thr Met Met Ser Gln Ile Phe Cys Gln His Ile Ser Pro
1025                1030                1035                1040
Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe Leu
                1045                1050                1055
Ile Arg Thr Ala Lys Ile Gln Gln Leu Val Cys Glu Thr Ile Val Arg
            1060                1065                1070
Val Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu
            1075                1080                1085
Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met
    1090                1095                1100
Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Val Pro
1105                1110                1115                1120
Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr
            1125                1130                1135
Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
            1140                1145                1150
Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn
    1155                1160                1165
Ser Ser Leu Pro Thr Ala Glu Thr Ile Tyr Thr Ile Tyr Glu Ile Ile
    1170                1175                1180
Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn
1185                1190                1195                1200
His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu
                1205                1210                1215
Asp Lys Leu Ser Gln Val Tyr Val Ile Leu Tyr Asp Ala Val Thr Glu
            1220                1225                1230
Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu
    1235                1240                1245
Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly
    1250                1255                1260
Asp Leu Gln Asp Leu Thr Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys
1265                1270                1275                1280
Thr Gly Val Ala Gln Leu Val Lys Tyr Ser Leu Lys Asp Leu Glu Asp
```

20

```
                    1285                    1290                    1295
      Val Val Gly Leu Leu Lys Lys Leu Gly Val Lys Leu Gln Val Ser Ile
                    1300                    1305                    1310
      Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Thr Gly Ile Ile Phe
                    1315                    1320                    1325
      Gln Phe Leu Ala Phe Ser Lys Arg Arg Gln Arg Val Val Pro Glu Ile
                    1330                    1335                    1340
      Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Lys Phe Arg Gly
      1345                    1350                    1355                    1360
      Pro Gln Thr Val Gly Pro Val Pro Thr Ala Val Gly Val Ser Ile Ala
                    1365                    1370                    1375
      Ile Asp Lys Ile Phe Ala Val Val Leu Asn Met Glu Glu Pro Val Thr
                    1380                    1385                    1390
      Val Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser Met
                    1395                    1400                    1405
      Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr
      1410                    1415                    1420
      Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu
      1425                    1430                    1435                    1440
      Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys
                    1445                    1450                    1455
      Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr
                    1460                    1465                    1470
      Glu Lys Arg Val Leu Glu Ser Asp Leu Val Asp His Val Met Gln Lys
                    1475                    1480                    1485
      Leu Arg Thr Lys Val Gly Asp Glu Arg Asn Phe Arg Asp Ala Ser Asp
                    1490                    1495                    1500
      Asn Leu Ala Val Gln Thr Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly
      1505                    1510                    1515                    1520
      Leu Phe Glu Ile His Gly Thr Thr Val Val Pro Asn Val Ile Val Leu
                    1525                    1530                    1535
      Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg His Glu Ile Gln
                    1540                    1545                    1550
      Val Gln Thr Arg Leu Gln Thr Thr Leu Ala Asn Leu His Gln Lys Ser
      1555                    1560                    1565
      Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu
      1570                    1575                    1580
      Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr
      1585                    1590                    1595                    1600
      Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys
                    1605                    1610                    1615
      Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser
                    1620                    1625                    1630
      Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
                    1635                    1640                    1645
```

<210> 6
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(270)
<223> Xaa = Any Amino Acid

21

<400> 6
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa
 1   5   10   15
Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa
                20   25   30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            35   40   45
Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        50   55   60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65   70   75   80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                100   105   110
Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Arg Asp
            115   120   125
Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        130   135   140
Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Asp Phe Gly Xaa Xaa Xaa Xaa
145   150   155   160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                165   170   175
Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp
        180   185   190
Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195   200   205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        210   215   220
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225   230   235   240
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa
                245   250   255
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa
            260   265   270

<210> 7
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(30)
<223> Xaa = Any Amino Acid

<400> 7
Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
                20   25   30

<210> 8
<211> 105

22

<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 8
Ile Leu Lys Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys
1   5   10   15
Arg Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp
            20   25   30
Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp
            35   40   45
Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala
    50   55   60
Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser
65   70   75   80
Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
            85   90   95
Glu Asn Gly Thr Val Lys Ile Ala Asp
            100   105

<210> 9
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 9
Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu
1   5   10   15
Lys Lys Cys Leu Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr
            20   25   30
Ala Lys Glu Ile Leu Asn His Pro Gln Phe
            35   40

<210> 10
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 10
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
1   5   10   15
Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
            20   25   30
Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
            35   40   45
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
    50   55   60
His Leu
65

23

<210> 11
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 11
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
1   5   10   15
Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
            20   25   30
Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
            35   40   45
Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
        50   55   60
Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
65   70   75   80
Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
                85   90   95
Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
            100   105   110
Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
        115   120   125
Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
    130   135   140
Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
145   150   155   160
Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
                165   170   175
Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
            180   185   190
Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
            195   200   205
Leu Asn His Pro Gln Phe
            210

<210> 12
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 12
Thr Asp Ile Ile Lys Tyr Pro Val Ile Thr Glu Lys Leu Ala Met Asn
1   5   10   15
Leu Leu Glu Glu Pro Asn Lys
            20

<210> 13
<211> 504
<212> PRT
<213> Artificial Sequence

24

<220>
<223> Consensus kinase sequence

<400> 13
Asn Gln Thr Thr Glu Arg Val Tyr Glu Leu His Lys Ile Glu Leu Phe
1   5   10   15
Ser Val Pro Glu Leu Asn Gly Lys Lys Ile Gly Leu Gly Ile Lys Leu
            20   25   30
Pro Lys Thr Asp Thr Glu Ser Leu Arg Thr Met Val Ala Lys Leu Leu
            35   40   45
Gly Leu Ala Met Lys Thr Lys Thr Phe Pro Asp Asp Glu Gly Ser Gln
    50   55   60
Pro Val Ser Phe Glu Arg Lys Asp Leu Glu Glu Ser Leu Lys Glu Lys
65   70   75   80
Asp Tyr Phe Val Cys Glu Lys Thr Asp Gly Ile Arg Cys Ser His Gly
                85   90   95
Phe Asn Arg Thr Gly Phe Leu Ile Ala Ala Leu Leu Phe Leu Val Glu
            100   105   110
His Pro Gly Leu Glu Glu Ala Ile Ser His Ile Leu Ser Gly Glu Phe
            115   120   125
Leu Ile Asp Arg Glu Lys Asn Tyr Tyr Lys Gln Asp Tyr Ile Asp Leu
    130   135   140
Leu Pro Lys Arg Leu Phe Pro Arg Glu Lys Asp Lys Thr Lys Ala Lys
145   150   155   160
Glu Leu Pro Thr Tyr His Arg Gly Thr Leu Leu Asp Gly Glu Leu Val
            165   170   175
Ile Asp Ile Asn Arg Ile Ala Val Glu Gln Lys Thr Leu Arg Tyr Val
            180   185   190
Val Phe Asp Ala Leu Ala Ile Ser Gly Gln Thr Val Ile Gln Arg Asp
    195   200   205
Leu Ser Lys Arg Leu Gly Asp Glu Phe Ile Lys Ala Val Lys Lys Pro
    210   215   220
Phe Asp Glu Phe Lys Lys Val Met Pro Asp Ala Lys Ile Leu Asn Gln
225   230   235   240
Gln Lys Tyr Asn Phe Pro Phe Lys Ile Gly Leu Lys His Met Ser Leu
            245   250   255
Ser Tyr Gly Gln Leu Lys Leu Leu Lys Ala Glu Ser Lys Met Val Ile
            260   265   270
Ser Lys Ala Asp Ala Met Pro Lys Leu Leu His Ile Asn Asp Gly Leu
    275   280   285
Ile Phe Thr Cys Val Arg Asp Thr Pro Tyr Ile Glu Gly Glu Ile Leu
    290   295   300
Val Glu Pro Gly Asn Ser Tyr Leu Asp Phe Asn Leu Leu Lys Trp Lys
305   310   315   320
Pro Lys Glu Glu Asn Thr Val Asp Phe Glu Leu Ile Leu Glu Phe Glu
            325   330   335
Glu Val Asn Asp Pro Glu Leu Asp Glu Lys Asp Gly Phe Ser Leu Tyr
            340   345   350
Leu Asp Tyr Asp Ala Met Pro Gly Glu Leu Phe Lys Phe Ser Leu Gly
    355   360   365
Val Trp Gln Gly Gly Phe Asn Lys Arg Phe Glu Val Ile His Thr Asp
    370   375   380
Gln Ile Phe Phe Arg Val Ala Phe Gln Lys Leu Gly Arg Leu Lys His
385   390   395   400
Glu Phe Ala Glu Leu Ser Val Ser Asp Lys Asp Trp Tyr Lys Leu Lys
            405   410   415

25

```
Ala Leu Glu Gln Pro Leu Asp Gly Arg Ile Val Glu Cys Arg Leu Ala
            420                 425                 430
Asp Ile Glu Ile Leu Ile Phe Gln Glu Gly Arg Trp Glu Tyr Leu Arg
        435                 440                 445
Phe Arg Asp Asp Lys Gln Gln Ala Leu Lys Thr Gly Gly Tyr Ser Gly
    450                 455                 460
Asn His Ile Ser Thr Val Glu Lys Val Leu Leu Ser Ile Lys Asp Gly
465                 470                 475                 480
Val Ser Ile Glu Glu Leu Leu Lys Leu Phe Pro Gly Met Tyr Phe Ala
                485                 490                 495
Gly Ala Lys Thr Leu Ile Lys Arg
            500
```

<210> 14
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 14
```
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
  1               5                 10                  15
Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
            20                  25                  30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
            35                  40                  45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
    50                  55                  60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65                  70                  75                  80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
            85                  90                  95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
            100                 105                 110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
            115                 120                 125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
    130                 135                 140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145                 150                 155                 160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
                165                 170                 175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
            180                 185                 190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
            195                 200                 205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
    210                 215                 220
Ile Lys Ala His Pro Phe Phe
225                 230
```

<210> 15
<211> 231
<212> PRT
<213> Artificial Sequence

26

<220>
<223> Consensus kinase sequence

<400> 15
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
1   5   10   15
Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
            20   25   30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
            35   40   45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
        50   55   60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65   70   75   80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
            85   90   95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
            100   105   110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
        115   120   125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
    130   135   140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145   150   155   160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
            165   170   175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
        180   185   190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
        195   200   205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
    210   215   220
Ile Lys Ala His Pro Phe Phe
225   230

<210> 16
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 16
Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
1   5   10   15
Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
            20   25   30
Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
        35   40   45
Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
    50   55   60
Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
65   70   75   80
Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
                85   90   95

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```
Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
            100                     105                 110
Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
            115                     120                 125
Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
            130                     135                 140
Gly Leu Ser Arg Asp Leu Tyr Asp Asp Asp Lys Lys Gly Glu Ser Lys
145                     150                     155                 160
Asp Tyr Tyr Arg Lys Lys Gly Gly Lys Gly Gly Lys Thr Leu Leu Pro
                165                     170                     175
Ile Arg Trp Met Ala Pro Glu Ser Leu Lys Asp Gly Lys Phe Thr Ser
                180                     185                     190
Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
            195                     200                     205
Leu Gly Glu Gln Pro Tyr Pro Gly Glu Ile Gln Gln Phe Met Ser Asn
            210                     215                     220
Glu Glu Val Leu Glu Tyr Leu Lys. Lys Gly Tyr Arg Leu Pro Lys Pro
225                     230                     235                 240
Glu Asn Asp Leu Pro Ile Ser Ser Val Thr Cys Pro Asp Glu Leu Tyr
                245                     250                     255
Asp Leu Met Leu Gln Cys Trp Ala Glu Asp Pro Glu Asp Arg Pro Thr
            260                     265                     270
Phe Ser Glu Leu Val Glu Arg Leu
            275                     280


<210> 17
<211> 144
<212> PRT
<213> Artificial Sequence


<220>
<223> Consensus kinase sequence


<400> 17
Ser Phe Arg Glu Arg Gln Ala Gln Glu Leu Glu Val Ile Lys Ser Ile
  1             5                   10                  15
Phe Gly Cys Asp Val Glu Asp Leu Arg Pro Gln Ala Asn Pro Ser Leu
            20                  25                  30
Trp Lys Pro Thr Asp Ile Arg Ile Gln Leu Thr Pro Leu Arg Asp Ser
            35                  40                  45
Ser Asn Gly Leu Glu Thr Tyr Val Cys Thr Lys Leu His Val Thr Cys
        50                  55                  60
Pro Ser Lys Tyr Pro Lys Leu Pro Pro Lys Ile Ser Leu Glu Glu Ser
65                  70                  75                  80
Lys Gly Met Ser Asp Gln Leu Leu Glu Ala Leu Arg Asn Gln Leu Gln
                85                  90                  95
Ala Gln Ser Gln Glu Leu Arg Gly Glu Val Met Ile Tyr Glu Leu Ala
            100                 105                 110
Gln Thr Val Gln Ala Phe Leu Leu Glu His Asn Lys Pro Pro Lys Gly
            115                 120                 125
Ser Phe Tyr Asp Gln Met Leu Gln Asp Lys Gln Lys Arg Asp Gln Glu
            130                 135                 140


<210> 18
<211> 54
<212> PRT
<213> Artiicial sequence
```

28

<220>
<223> Consensus kinase sequence

<400> 18
Glu Thr Leu Tyr Phe His Lys Met Gly Arg Gln Ile Gln Arg Gly Cys
1   5   10   15
Cys Val Gly His Ser Gln Arg Gly Cys Ile Ala Tyr Thr Gly Ile Asp
                20   25   30
Met His Cys Gly Gln Leu Leu Tyr Ile Thr Glu Trp Asn Ile Lys Tyr
            35   40   45
Ser Gln Leu Glu Gln Pro
        50

<210> 19
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 19
Leu Lys Ser Leu Met Arg Gly Lys Gly Glu Ala Ala Ser Leu Ala Arg
1   5   10   15
Gly Ala Leu Arg Glu Leu Glu Thr Val Val Gly Leu Ala Tyr Ser Leu
                20   25   30
Gly Val Lys Cys Pro Ile His Ile Trp Ala Gly Leu Pro Ile Ser Phe
            35   40   45
Asp Arg Ala Ser Asn Gly Gly Ile Val Trp Gln Met Thr Ala Asp Leu
        50   55   60
Lys Pro Asn Arg Ser Gly His Pro Ser Val Leu Ala Ile Gly Glu Arg
65   70   75   80
Tyr Asp Ser Met Leu His Glu Phe Gln Lys Gln Ala Gln Lys Phe Asn
                85   90   95
Pro Ala Met Pro Ala Arg Gly Val Leu Ser Gly Ala Gly Leu Thr Phe
                100   105   110
Ser Leu Asp Lys Leu Val Ala Ala Val Gly Val Glu Tyr Ala Lys Asp
            115   120   125
Cys Arg Ala Ile Asp Val Gly Ile Cys Val Cys Gly Thr Arg Pro Pro
        130   135   140
Leu Lys Asp Val Thr Tyr Ile Met Arg Leu Leu Trp Ser Val Gly Ile
145   150   155   160
Arg Cys Gly Ile Val Glu Ala Ala Ser Glu Leu Gly Asp Glu Ala Gln
                165   170   175
Asp Leu Ala Arg Leu Gly Ala Leu His Val Ile Leu Val Ala Glu Asn
            180   185   190
Gly Ser Leu Arg Val Arg Ser Phe Glu Arg Glu Arg Phe Gln Glu Arg
        195   200   205
His Leu Thr Arg Thr Glu Leu Val Glu Phe Ile Gln Lys Met Leu Arg
    210   215   220
Ser Asp Gly Leu Asn Gly Thr Thr Val Asp Asn Phe Ser His Leu Ser
225   230   235   240
Ala Leu Gly Ser Gly Asp Asn Arg Ser Ser Gly Gly Lys Glu Arg Glu
                245   250   255
Arg Gly Glu Asn Gly Leu Ser Thr Ser Ala Ser Asn Ala Thr Ile Lys
                260   265   270

29

```
Asn Asn Tyr Ser Gln Leu Pro Asn Leu Gln Val Thr Phe Leu Thr His
        275             280             285
Asp Lys Pro Thr Ala Asn Tyr Lys Arg Arg Leu Glu Asn Gln Val Ala
        290             295             300
Gln Gln Met Ser Ser Thr Leu Ser Gln Phe Leu Lys Lys Glu Thr Phe
305             310             315             320
Val Val Leu Val Val Glu Leu Pro Pro Ala Val Val
                325             330
```

<210> 20
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 20
```
Val Leu Ser Gly Ala Gly Leu Thr Phe Ser Leu Asp Lys Leu Val Ala
1               5               10              15
Ala Val Gly Val Glu Tyr Ala Lys Asp Cys Arg Ala Ile Asp Val Gly
        20              25              30
Ile Cys Val Cys Gly Thr Arg Pro Pro Leu Lys Asp Val Thr Tyr Ile
        35              40              45
Met Arg Leu Leu Trp Ser Val Gly Ile Arg Cys Gly Ile Val Glu Ala
        50              55              60
Ala Ser Glu Leu Gly Asp Glu Ala Gln Asp Leu Ala Arg Leu Gly Ala
65              70              75              80
Leu His Val Ile Leu Val Ala Glu Asn Gly Ser Leu Arg Val Arg Ser
                85              90              95
Phe Glu Arg Glu Arg Phe Gln Glu Arg His Leu Thr Arg Thr Glu Leu
        100             105             110
Val Glu Phe Ile Gln Lys Met Leu Arg Ser Asp Gly Leu Asn Gly Thr
        115             120             125
Thr Val Asp Asn Phe Ser His Leu Ser Ala Leu Gly Ser Gly Asp Asn
        130             135             140
Arg Ser Ser Gly Gly Lys Glu Arg Glu Arg Gly Glu Asn Gly Leu Ser
145             150             155             160
Thr Ser Ala Ser Asn Ala Thr Ile Lys Asn Asn Tyr Ser Gln Leu Pro
                165             170             175
Asn Leu Gln Val Thr Phe Leu Thr His Asp Lys Pro Thr Ala Asn Tyr
                180             185             190
Lys Arg Arg Leu Glu Asn Gln Val Ala Gln Gln Met Ser Ser Thr Leu
        195             200             205
Ser Gln Phe Leu Lys Lys Glu Thr Phe Val Val Leu Val Val Glu Leu
        210             215             220
Pro Pro Ala Val Val Asn Ala Ile Val Gly Ala Ile Asn Pro Arg Glu
225             230             235             240
Ile Arg Lys Arg Glu Thr Glu Pro Glu Ile Asn Tyr Val Ile Glu Arg
                245             250             255
Phe Ser Lys Tyr Lys Arg Tyr Ile Ser Glu Ile Asn Glu Glu Val Val
                260             265             270
Asp Tyr Leu Ser Asp Ala Lys Thr Pro Ile Val Ala Leu Tyr Ser Ile
        275             280             285
Ser Asp Ser Tyr Tyr Arg Val Ile
290             295
```

<210> 21
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 21
Asp Gln Gly Gly Glu Leu Leu Ser Leu Arg Tyr Asp Leu Thr Val Pro
  1   5   10   15
Phe Ala Arg Tyr Val Ala Met Asn Leu Leu Lys Val Thr Asn Leu Pro
             20   25   30
Leu Lys Arg Tyr His Ile Ala Lys Val Tyr Arg Arg Asp Arg Pro Ala
             35   40   45
Met Thr Arg Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp Phe Asp Ile
        50   55   60
Ile Gly Glu Tyr Asp Thr Met Ala Pro Asp Ala Glu Ile Leu Lys Ile
65   70   75   80
Leu Thr Glu Ile Leu Ser Gln Leu Gly Ile Arg Glu Leu Gly Asn Phe
                85   90   95
Lys Ile Lys Ile Asn His Arg Gly Ile Leu Asp Ser Leu Leu Gln Pro
            100   105   110
Trp Pro Lys Thr Leu Gln Glu Tyr Leu Thr Gln Tyr Lys Ala
            115   120   125

<210> 22
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 22
Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu Asn
  1   5   10   15
Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys Glu
             20   25   30
Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln Ala
             35   40   45
Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro Tyr
        50   55   60
Tyr Val Ser Met Lys Ser Met Ala Pro Glu Tyr Met Ala Pro Glu Ser
65   70   75   80
Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr Lys Ser Asp Val Trp Ser
                85   90   95
Phe Gly Val Ile Leu Tyr Glu Met
            100

<210> 23
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

31

<400> 23

```
Gln Leu Met His Tyr Val His Gln Ile Ala Lys Gly Leu Glu Tyr Leu
1               5                   10                  15
His Ser Lys Asn Gln Lys His Gln Gly Ile Ile His Arg Ala Lys Lys
            20                  25                  30
Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu
            35                  40                  45
Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys
        50                  55                  60
Glu Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln
65                  70                  75                  80
Ala Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro
                85                  90                  95
Tyr Tyr Val Ser
            100
```

<210> 24
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 24

```
Glu Gly Ser Leu Val Glu Tyr Met Glu Tyr Met Ser Gly Gly Ser Glu
1               5                   10                  15
Asp Tyr Met Lys Lys Leu Ser Leu Glu Thr Val Met Lys Ile Ala Met
            20                  25                  30
Met Ile Leu Gln Phe Met Gln Ile Met His Met Ser Ser Glu Ser Glu
        35                  40                  45
Ser Leu Ser His Ser Gln Leu Met His Tyr Val His Gln Ile Ala Lys
        50                  55                  60
Gly Leu Glu Tyr Leu His Ser Lys Asn Gln Lys His Gln Gly Ile Ile
65                  70                  75                  80
His Arg Ala Lys Lys Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
                85                  90                  95
Glu Glu Ser His Glu Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp
                100                 105                 110
Phe Gly Leu Ala Lys Glu Ile
            115
```

<210> 25
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 25

```
Tyr Met Ala Pro Glu Ser Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr
1               5                   10                  15
Lys Ser Asp Val Trp Ser Phe Gly Val Ile Leu Tyr Glu Met Leu Thr
            20                  25                  30
Gly Lys Pro Pro Phe Phe Pro Gly Glu Ser Glu Val Ser Glu Glu Glu
```

```
              35                      40                      45
Pro Tyr Gln Ser Met Lys Asn Met Glu Val Leu Glu Met Gly Pro Glu
         50                      55                      60
Glu Thr Ile Gln Lys Val Met Ser Lys Ile Val Glu Lys Lys Gly Glu
65                      70                      75                      80
Arg Met Pro Gln Pro Ser Ser Ser Asn Cys Pro Glu Val Ser Gln Glu
                   85                      90                      95
Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys Asp Pro Glu Lys Arg
                 100                     105                     110
Arg Pro Thr Phe Glu Glu Ile Leu Gln His
                 115                     120
```

<210> 26
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 26
```
Gln Tyr Glu Leu Leu Lys Lys Leu Leu Gly Lys Gly Ser Phe Gly Lys
 1               5                      10                      15
Val Tyr Lys Ala Lys His Lys
              20
```

<210> 27
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 27
```
Glu Val Ser Gln Glu Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys
 1               5                      10                      15
Asp Pro Glu Lys Arg Arg Pro Thr Phe Glu Glu Ile Leu Gln His Pro
              20                      25                      30
Trp Phe Leu Met Arg Asn Pro
              35
```

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 28
```
Leu Gly Thr Gly Ser Phe Gly Ala Val Tyr Lys
 1               5                      10
```

<210> 29
<211> 104
<212> PRT

<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 29
Leu Asp Gln Asn Gly Thr Val Leu Gln Leu Pro Phe Asp Leu Met Met
1   5   10   15
Gly His Ala Arg Ser Leu Ala Arg Ile Thr Asn Ser Pro Val Val Gln
                20   25   30
Lys Ser Tyr Ser Phe Gly Asn Ile Phe Arg Asp Arg His Gly Gly Gly
        35   40   45
Gln Pro Asp Val Tyr Gly Glu Val Asp Phe Asp Ile Val Thr Ser Asp
    50   55   60
Ala Leu Asp Leu Ala Leu Lys Glu Ala Glu Val Ile Lys Val Leu Asp
65   70   75   80
Glu Ile Ala Thr Ala Phe Pro Thr Val Ser Ser Thr Pro Ile Cys Phe
                85   90   95
Gln Leu Gly His Ser Asp Leu Leu
                100

<210> 30
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 30
Tyr Gln Glu Val Gln Glu Ser Glu Val Met Val Leu Gln Ala Ile Tyr
1   5   10   15
Gly Glu Asp Phe Thr Gln His Glu Ala Ala His Gly Ala Trp Gln Lys
                20   25   30
Ser Glu Pro Arg Phe Asp Ile Lys Ile Lys Pro Ser Ser Asp Gln Glu
        35   40   45
Leu Ser Val Thr Leu Gly Val Val Met Val Ala Thr Tyr Pro Lys Thr
    50   55   60
Pro Pro Leu Leu Thr Ile Lys Asp Asp His Ser Leu Arg Glu Ser Thr
65   70   75   80
Lys Phe Lys Ile Gln Lys Phe Val Glu Thr Gln Pro Lys Ile Tyr Ala
                85   90   95
Gln Ala Glu Gln Glu Met Ile Asp Gln Ile Val Glu Gly Ile Arg Asp
                100   105   110
Ile Leu Glu Glu Ala Ala Gln Lys Lys Val Gln Gly Leu Glu Ile Pro
        115   120   125
Ser Leu Glu Glu Glu Arg Ala Ala His Glu Ala Glu Leu Ala Arg Leu
    130   135   140
Ala Gln Ser Glu Lys Glu Arg
145   150

<210> 31
<211> 48
<212> PRT
<213> Artificial Sequence

<220>

34

<223> Consensus kinase sequence

<400> 31
Glu Ala Glu Leu Ala Arg Leu Ala Gln Ser Glu Lys Glu Arg Glu Glu
1   5   10   15
Arg Lys Lys Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp
            20   25   30
Met Leu Gln Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser
        35   40   45

<210> 32
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 32
Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys Asn Arg Ser His Gln Leu
1   5   10   15
Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly Glu Thr Asp Glu Thr Leu
            20   25   30
Met Phe Asp Gln Pro Cys Lys Ile Thr Asp Gly Ser Gly Asn Ala Leu
        35   40   45
Phe Phe Gln Thr Val Ile Gly Lys Thr Val Phe
        50   55

<210> 33
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 33
Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp Met Leu Gln
1   5   10   15
Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys
            20   25   30
Asn Arg Ser His Gln Leu Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly
        35   40   45
Glu Thr Asp Glu Thr Leu Met Phe Asp Gln Pro Cys Lys Ile Thr Asp
        50   55   60
Gly Ser Gly Asn Ala Leu Phe Phe Gln Thr Val Ile Gly Lys Thr Val
65   70   75   80
Phe Arg Glu